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Sequence Listing was accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: markspencer
Timestamp: [year=2008; month=8; day=29; hr=14; min=36; sec=42; ms=293; ]
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Validated By CRFValidator v 1.0.3

Application No: 10501566   Version No: 4.0

Input Set:

Output Set:

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Finished: 2008-07-28 16:24:09.991
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 41 ms
Total Warnings: 178
Total Errors: 0
No. of SeqIDs Defined: 178
Actual SeqID Count: 178

Error code   Error Description

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W   402   Undefined organism found in <213> in SEQ ID (2)

W   213   Artificial or Unknown found in <213> in SEQ ID (3)

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W   213   Artificial or Unknown found in <213> in SEQ ID (5)

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              Input Set:


             Output Set:



              Started:  2008-07-28 16:24:05.950
             Finished:  2008-07-28 16:24:09.991
              Elapsed:  0 hr(s) 0 min(s) 4 sec(s) 41 ms
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Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (28) This error has occured more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (39)
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        HIKICHI, Yukiko
        SAGIYA, Yoji
        NAKANISHI, Atsushi

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Val Phe Thr Val Val Ser Thr Val Met Met Gly Leu Leu Met Phe Ser
            35   40   45
Leu Gly Cys Ser Val Glu Ile Arg Lys Leu Trp Ser His Ile Arg Arg
        50   55   60
Pro Trp Gly Ile Ala Val Gly Leu Leu Cys Gln Phe Gly Leu Met Pro

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Phe Thr Ala Tyr Leu Leu Ala Ile Ser Phe Ser Leu Lys Pro Val Gln
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                  100                   105                   110
Asn Ile Phe Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
        115                   120                   125
Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
      130                   135                   140
Ile Tyr Leu Tyr Thr Trp Ser Trp Ser Leu Gln Gln Asn Leu Thr Ile
145                   150                   155                   160
Pro Tyr Gln Asn Ile Gly Ile Thr Leu Val Cys Leu Thr Ile Pro Val
                  165                   170                   175
Ala Phe Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ser Lys Ile
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Ile Leu Lys Ile Gly Ala Val Val Gly Gly Val Leu Leu Leu Val Val
             195                   200                   205
Ala Val Ala Gly Val Val Leu Ala Lys Gly Ser Trp Asn Ser Asp Ile
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Thr Leu Leu Thr Ile Ser Phe Ile Phe Pro Leu Ile Gly His Val Thr
225                   230                   235                   240
Gly Phe Leu Leu Ala Leu Phe Thr His Gln Ser Trp Gln Arg Cys Arg
                  245                   250                   255
Thr Ile Ser Leu Glu Thr Gly Ala Gln Asn Ile Gln Met Cys Ile Thr
             260                   265                   270
Met Leu Gln Leu Ser Phe Thr Ala Glu His Leu Val Gln Met Leu Ser
        275                   280                   285
Phe Pro Leu Ala Tyr Gly Leu Phe Gln Leu Ile Asp Gly Phe Leu Ile
      290                   295                   300
Val Ala Ala Tyr Gln Thr Tyr Lys Arg Arg Leu Lys Asn Lys His Gly
305                   310                   315                   320
Lys Lys Asn Ser Gly Cys Thr Glu Val Cys His Thr Arg Lys Ser Thr
                  325                   330                   335
Ser Ser Arg Glu Thr Asn Ala Phe Leu Glu Val Asn Glu Glu Gly Ala
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<213> Human


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atgatggggc tgctcatgtt ctctttggga tgttccgtgg agatccggaa gctgtggtcg   180
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atgccactct gcatttatct ctacacctgg tcctggagtc ttcagcagaa tctcaccatt   480
ccttatcaga acataggaat tacccttgtg tgcctgacca ttcctgtggc ctttggtgtc   540
tatgtgaatt acagatggcc aaaacaatcc aaaatcattc tcaagattgg ggccgttgtt   600
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accaatgcct tcttggaggt gaatgaagaa ggtgccatca ctcctgggcc accagggcca     1080
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<220>
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<220>
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<400> 5
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<220>
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atgatggggc tgctcatgtt ctctttggga tgttccgtgg agatccggaa gctgtggtcg   180
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ctagctggct gg                                                         1152


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<212> DNA
<213> Human

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atgatggggc tgctcatgtt ctctttggga tgttccgtgg agatccggaa gctgtggtcg      180
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                 20                  25                  30
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             35                  40                  45
Leu Gly Cys Ser Val Glu Ile Arg Lys Leu Trp Ser His Ile Arg Arg
         50                  55                  60
Pro Trp Gly Ile Ala Val Gly Leu Leu Cys Gln Phe Gly Leu Met Pro
 65                  70                  75                  80
Phe Thr Ala Tyr Leu Leu Ala Ile Ser Phe Ser Leu Lys Pro Val Gln
                 85                  90                  95
Ala Ile Ala Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Ile Ser
                100                 105                 110
Asn Val Phe Thr Phe Trp Val Asp Gly Asp Met Asp Leu Ser Ile Ser
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Met Thr Thr Cys Ser Thr Val Ala Ala Leu Gly Met Met Pro Leu Cys
         130                 135                 140
Ile Tyr Leu Tyr Thr Trp Ser Trp Ser Leu Gln Gln Asn Leu Thr Ile
145                 150                 155                 160
Pro Tyr Gln Asn Ile Gly Ile Thr Leu Val Cys Leu Thr Ile Pro Val
                165                 170                 175
Ala Phe Gly Val Tyr Val Asn Tyr Arg Trp Pro Lys Gln Ser Lys Ile
             180                 185                 190
Ile Leu Lys Ile Gly Ala Val Val Gly Gly Val Leu Leu Leu Val Val
             195                 200                 205
Ala Val Ala Gly Val Val Leu Ala Lys Gly Ser Trp Asn Ser Asp Ile
         210                 215                 220
Thr Leu Leu Thr Ile Ser Phe Ile Phe Pro Leu Ile Gly His Val Thr
225                 230                 235                 240
Gly Phe Leu Leu Ala Leu Phe Thr His Gln Ser Trp Gln Arg Cys Arg
                245                 250                 255
Thr Ile Ser Leu Glu Thr Gly Ala Gln Asn Ile Gln Met Cys Ile Thr
                260                 265                 270
Met Leu Gln Leu Ser Phe Thr Ala Glu His Leu Val Gln Met Leu Ser
             275                 280                 285
Phe Pro Leu Ala Tyr Gly Leu Phe Gln Leu Ile Asp Gly Phe Leu Ile
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Val Ala Ala Tyr Gln Thr Tyr Lys Arg Arg Leu Lys Asn Lys His Gly
305                 310                 315                 320
Lys Lys Asn Ser Gly Cys Thr Glu Val Cys His Thr Arg Lys Ser Thr
                325                 330                 335
Ser Ser Arg Glu Thr Asn Ala Phe Leu Glu Val Asn Glu Glu Gly Ala
             340                 345                 350
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<210> 17
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<213> Human

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            20   25   30
Ser Ala Asn Ser Thr Ala Gln Tyr Ala Ser Asn Ala Trp Phe Ala Ala
        35   40   45
Ala Ser Ser Glu Pro Glu Glu Gly Ile Ser Val Phe Glu Leu Asp Tyr
    50   55   60
Asp Tyr Val Gln Ile Pro Tyr Glu Val Thr Leu Trp Ile Leu Leu Ala
65   70   75   80
Ser Leu Ala Lys Ile Gly Phe His Leu Tyr His Arg Leu Pro Gly Leu
                85   90   95
Met Pro Glu Ser Cys Leu Leu Ile Leu Val Gly Ala Leu Val Gly Gly
            100   105   110

Ile Ile Phe Gly Thr Asp His Lys Ser Pro Pro Val Met Asp Ser Ser
        115   120   125
Ile Tyr Phe Leu Tyr Leu Leu Pro Pro Ile Val Leu Glu Gly Gly Tyr
        130   135   140
Phe Met Pro Thr Arg Pro Phe Phe Glu Asn Ile Gly Ser Ile Leu Trp
145   150   155   160
Trp Ala Val Leu Gly Ala Leu Ile Asn Ala Leu Gly Ile Gly Leu Ser
                165   170   175
Leu Tyr Leu Ile Cys Gln Val Lys Ala Phe Gly Leu Gly Asp Val Asn
                180   185   190
Leu Leu Gln Asn Leu Leu Phe Gly Ser Leu Ile Ser Ala Val Asp Pro
                195   200   205
Val Ala Val Leu Ala Val Phe Glu Glu Ala Arg Val Asn Glu Gln Leu
        210   215   220
Tyr Met Met Ile Phe Gly Glu Ala Leu Leu Asn Asp Gly Ile Thr Val
225   230   235   240
Val Leu Tyr Asn Met Leu Ile Ala Phe Thr Lys Met His Lys Phe Glu
                245   250   255
Asp Ile Glu Thr Val Asp Ile Leu Ala Gly Cys Ala Arg Phe Ile Val
                260   265   270
Val Gly Leu Gly Gly Val Leu Phe Gly Ile Val Phe Gly Phe Ile Ser
        275   280   285
Ala Phe Ile Thr Arg Phe Thr Gln Asn Ile Ser Ala Ile Glu Pro Leu
        290   295   300
Ile Val Phe Met Phe Ser Tyr Leu Ser Tyr Leu Ala Ala Glu Thr Leu
305   310   315   320
Tyr Leu Ser Gly Ile Leu Ala Ile Thr Ala Cys Ala Val Thr Met Lys
                325   330   335
Lys Tyr Val Glu Glu Asn Val Ser Gln Thr Ser Tyr Thr Thr Ile Lys
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Tyr Phe Met Lys Met Leu Ser Ser Val Ser Glu Thr Leu Ile Phe Ile
        355   360   365
Phe Met Gly Val Ser Thr Val Gly Lys Asn His Glu Trp Asn Trp Ala
        370   375   380
Phe Ile Cys Phe Thr Leu Ala Phe Cys Gln Ile Trp Arg Ala Ile Ser
385   390   395   400
Val Phe Ala Leu Phe Tyr Ile Ser Asn Gln Phe Arg Thr Phe Pro Phe
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